

SEQUENCE LISTING

<110> GLUCKSMANN, MARIA ALEXANDRA

<120> 93870, A HUMAN G-PROTEIN COUPLED
RECEPTOR AND USES THEREFOR

<130> MPI2001-021P1RCP1 (M)

<150> 60/272,677

<151> 2001-03-01

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147)...(1085)

<223> The nucleotide at position 1384 can be any
nucleotide

<400> 1

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tggaagttgt agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120
ttgatacacc aatcctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173
                               Met Gln Lys Cys Asp Phe Pro Ser Met
                               1           5
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cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
10           15           20           25
```

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ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
30           35           40
```

```
ggt gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
45           50           55
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gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
60           65           70
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ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
75           80           85
```

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atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
90           95           100           105
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cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga 509
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His	Met	Tyr	Leu	Thr	Phe	Leu	Phe	Tyr	Val	Val	Ile	Leu	Val	Thr	Arg	
				110					115					120		
tac	ctc	atc	ttc	ttc	aag	tgc	aaa	gac	aaa	gtg	gaa	ttc	tac	aga	aaa	557
Tyr	Leu	Ile	Phe	Phe	Lys	Cys	Lys	Asp	Lys	Val	Glu	Phe	Tyr	Arg	Lys	
			125					130					135			
ctg	cat	gct	gtg	gct	gcc	agt	gct	ggc	atg	tgg	acg	ctg	gtg	att	gtc	605
Leu	His	Ala	Val	Ala	Ala	Ser	Ala	Gly	Met	Trp	Thr	Leu	Val	Ile	Val	
		140					145					150				
att	gtg	gta	ccc	ctg	gtt	gtc	tcc	cgg	tat	gga	atc	cat	gag	gaa	tac	653
Ile	Val	Val	Pro	Leu	Val	Val	Ser	Arg	Tyr	Gly	Ile	His	Glu	Glu	Tyr	
	155					160					165					
aat	gag	gag	cac	tgt	ttt	aaa	ttt	cac	aaa	gag	ctt	gct	tac	aca	tat	701
Asn	Glu	Glu	His	Cys	Phe	Lys	Phe	His	Lys	Glu	Leu	Ala	Tyr	Thr	Tyr	
	170				175					180					185	
gtg	aaa	atc	atc	aac	tat	atg	ata	gtc	att	ttt	gtc	ata	gcc	gtt	gct	749
Val	Lys	Ile	Ile	Asn	Tyr	Met	Ile	Val	Ile	Phe	Val	Ile	Ala	Val	Ala	
				190					195					200		
gtg	att	ctg	ttg	gtc	ttc	cag	gtc	ttc	atc	att	atg	ttg	atg	gtg	cag	797
Val	Ile	Leu	Leu	Val	Phe	Gln	Val	Phe	Ile	Ile	Met	Leu	Met	Val	Gln	
			205					210					215			
aag	cta	cgc	cac	tct	tta	cta	tcc	cac	cag	gag	ttc	tgg	gct	cag	ctg	845
Lys	Leu	Arg	His	Ser	Leu	Leu	Ser	His	Gln	Glu	Phe	Trp	Ala	Gln	Leu	
		220					225					230				
aaa	aac	cta	ttt	ttt	ata	ggg	gtc	atc	ctt	gtt	tgt	ttc	ctt	ccc	tac	893
Lys	Asn	Leu	Phe	Phe	Ile	Gly	Val	Ile	Leu	Val	Cys	Phe	Leu	Pro	Tyr	
	235					240					245					
cag	ttc	ttt	agg	atc	tat	tac	ttg	aat	gtt	gtg	acg	cat	tcc	aat	gcc	941
Gln	Phe	Phe	Arg	Ile	Tyr	Tyr	Leu	Asn	Val	Val	Thr	His	Ser	Asn	Ala	
	250				255					260					265	
tgt	agc	agc	aag	gtt	gca	ttt	tat	aac	gaa	atc	ttc	ttg	agt	gta	aca	989
Cys	Ser	Ser	Lys	Val	Ala	Phe	Tyr	Asn	Glu	Ile	Phe	Leu	Ser	Val	Thr	
				270					275					280		
gca	att	agc	tgc	tat	gat	ttg	ctt	ctc	ttt	gtc	ttt	ggg	gga	agc	cat	1037
Ala	Ile	Ser	Cys	Tyr	Asp	Leu	Leu	Leu	Phe	Val	Phe	Gly	Gly	Ser	His	
			285					290					295			
tgg	ttt	aag	caa	aag	ata	att	ggc	tta	tgg	aat	tgt	gtt	ttg	tgc	cgt	1085
Trp	Phe	Lys	Gln	Lys	Ile	Ile	Gly	Leu	Trp	Asn	Cys	Val	Leu	Cys	Arg	
		300					305					310				
tagccacaaa	ctacagtatt	catatattgct	tcctttatat	tgggaataaaa	atgggtatag	1145										
gggaggtaag	aatggtat	cattacttga	tcaaaacccat	gccttgatgt	acccaaaaca	1205										
aaaggactat	aaaatgcaag	agccctcatt	gtagtcctta	tgggatccct	cccatctctg	1265										
agtgatggcc	gtacaaagac	cagtgttggt	gaatccacct	ggagttgcaa	tattacatta	1325										
ttttccagta	cagaatgtct	gtgtggccca	tgaagcaac	ataggtttta	agagtttttna	1385										
gagtttcatt	agctcattct	aagttcctct	gtttgaagca	tgggtctctta	ggttttggac	1445										
tgaactcaga	cctttagttc	ttttcatccc	acttcacccat	aggtaagtaa	attctggcca	1505										
ccacccagct	ccaaagacac	aaactctcct	tcgctaacca	ggtttagatgt	cccattcatc	1565										
tcatgccctg	ataaaaactg	ataaggggag	agaatagtta	aaaatttttc	taggggtatca	1625										
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<210> 2
<211> 313

<212> PRT
 <213> Homo sapiens

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 Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg
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 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
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 Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe
 35 40 45
 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile
 50 55 60
 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg
 65 70 75 80
 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys
 85 90 95
 Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu
 100 105 110
 Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys
 115 120 125
 Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser
 130 135 140
 Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val
 145 150 155 160
 Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys
 165 170 175
 Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met
 180 185 190
 Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln
 195 200 205
 Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu
 210 215 220
 Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly
 225 230 235 240
 Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr
 245 250 255
 Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe
 260 265 270
 Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu
 275 280 285
 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile
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 Gly Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

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 aat tcc tct tgc gat cct ata gtg aca ccc cac tta atc agc ctc tac 96
 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
 20 25 30

ttc	ata	gtg	ctt	att	ggc	ggg	ctg	gtg	ggt	gtc	att	tcc	att	ctt	ttc	144																																															
Phe	Ile	Val	Leu	Ile	Gly	Gly	Leu	Val	Gly	Val	Ile	Ser	Ile	Leu	Phe																																																
35																40																45																															
ctc	ctg	gtg	aaa	atg	aac	acc	cgg	tca	gtg	acc	acc	atg	gcg	gtc	att	192																																															
Leu	Leu	Val	Lys	Met	Asn	Thr	Arg	Ser	Val	Thr	Thr	Met	Ala	Val	Ile																																																
50																55																60																															
aac	ttg	gtg	gtg	gtc	cac	agc	gtt	ttt	ctg	ctg	aca	gtg	cca	ttt	cgc	240																																															
Asn	Leu	Val	Val	Val	His	Ser	Val	Phe	Leu	Leu	Thr	Val	Pro	Phe	Arg																																																
65																70																75																80															
ttg	acc	tac	ctc	atc	aag	aag	act	tgg	atg	ttt	ggg	ctg	ccc	ttc	tgc	288																																															
Leu	Thr	Tyr	Leu	Ile	Lys	Lys	Thr	Trp	Met	Phe	Gly	Leu	Pro	Phe	Cys																																																
85																90																95																															
aaa	ttt	gtg	agt	gcc	atg	ctg	cac	atc	cac	atg	tac	ctc	acg	ttc	cta	336																																															
Lys	Phe	Val	Ser	Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu																																																
100																105																110																															
ttc	tat	gtg	gtg	atc	ctg	gtc	acc	aga	tac	ctc	atc	ttc	ttc	aag	tgc	384																																															
Phe	Tyr	Val	Val	Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys																																																
115																120																125																															
aaa	gac	aaa	gtg	gaa	ttc	tac	aga	aaa	ctg	cat	gct	gtg	gct	gcc	agt	432																																															
Lys	Asp	Lys	Val	Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser																																																
130																135																140																															
gct	ggc	atg	tgg	acg	ctg	gtg	att	gtc	att	gtg	gta	ccc	ctg	gtt	gtc	480																																															
Ala	Gly	Met	Trp	Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val																																																
145																150																155																160															
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165																170																175																															
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Phe	His	Lys	Glu	Leu	Ala	Tyr	Thr	Tyr	Val	Lys	Ile	Ile	Asn	Tyr	Met																																																
180																185																190																															
ata	gtc	att	ttt	gtc	ata	gcc	gtt	gct	gtg	att	ctg	ttg	gtc	ttc	cag	624																																															
Ile	Val	Ile	Phe	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Leu	Val	Phe	Gln																																																
195																200																205																															
gtc	ttc	atc	att	atg	ttg	atg	gtg	cag	aag	cta	cgc	cac	tct	tta	cta	672																																															
Val	Phe	Ile	Ile	Met	Leu	Met	Val	Gln	Lys	Leu	Arg	His	Ser	Leu	Leu																																																
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Ser	His	Gln	Glu	Phe	Trp	Ala	Gln	Leu	Lys	Asn	Leu	Phe	Phe	Ile	Gly																																																
225																230																235																240															
gtc	atc	ctt	gtt	tgt	ttc	ctt	ccc	tac	cag	ttc	ttt	agg	atc	tat	tac	768																																															
Val	Ile	Leu	Val	Cys	Phe	Leu	Pro	Tyr	Gln	Phe	Phe	Arg	Ile	Tyr	Tyr																																																
245																250																255																															
ttg	aat	gtt	gtg	acg	cat	tcc	aat	gcc	tgt	agc	agc	aag	gtt	gca	ttt	816																																															
Leu	Asn	Val	Val	Thr	His	Ser	Asn	Ala	Cys	Ser	Ser	Lys	Val	Ala	Phe																																																
260																265																270																															
tat	aac	gaa	atc	ttc	ttg	agt	gta	aca	gca	att	agc	tgc	tat	gat	ttg	864																																															

ctt ctc ttt gtc ttt ggg gga agc cat tgg ttt aag caa aag ata att 912
 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile
 290 295 300

ggc tta tgg aat tgt gtt ttg tgc cgt 939
 Gly Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 4
 <211> 356
 <212> PRT
 <213> Mus muscalis

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 Asn Asp Phe Met Ser Gly Phe Leu Cys Phe Ser Ile Asn Val Arg Ala
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 Phe Gly Ile Thr Val Pro Thr Pro Leu Tyr Ser Leu Val Phe Ile Ile
 35 40 45
 Gly Val Ile Gly His Val Leu Val Val Leu Val Leu Ile Gln His Lys
 50 55 60
 Arg Leu Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser
 65 70 75 80
 Asp Leu Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met
 85 90 95
 Lys Gly Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly
 100 105 110
 Phe Tyr Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu
 115 120 125
 Thr Ile Asp Arg Tyr Leu Ala Val Val His Val Val Phe Ala Leu Arg
 130 135 140
 Ala Arg Thr Val Thr Phe Gly Ile Ile Ser Ser Ile Ile Thr Trp Val
 145 150 155 160
 Leu Ala Ala Leu Val Ser Ile Pro Cys Leu Tyr Val Phe Lys Ser Gln
 165 170 175
 Met Glu Phe Thr Tyr His Thr Cys Arg Ala Ile Leu Pro Arg Lys Ser
 180 185 190
 Leu Ile Arg Phe Leu Arg Phe Gln Ala Leu Thr Met Asn Ile Leu Gly
 195 200 205
 Leu Ile Leu Pro Leu Leu Ala Met Ile Ile Cys Tyr Thr Arg Ile Ile
 210 215 220
 Asn Val Leu His Arg Arg Pro Asn Lys Lys Lys Ala Lys Val Met Arg
 225 230 235 240
 Leu Ile Phe Val Ile Thr Leu Leu Phe Phe Leu Leu Ala Pro Tyr
 245 250 255
 Tyr Leu Ala Ala Phe Val Ser Ala Phe Glu Asp Val Leu Phe Thr Pro
 260 265 270
 Ser Cys Leu Arg Ser Gln Gln Val Asp Leu Ser Leu Met Ile Thr Glu
 275 280 285
 Ala Leu Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Val Phe
 290 295 300
 Val Gly Lys Arg Phe Arg Lys Tyr Leu Trp Gln Leu Phe Arg Arg His
 305 310 315 320
 Thr Ala Ile Thr Leu Pro Gln Trp Leu Pro Phe Leu Ser Glu Asp Arg
 325 330 335
 Ala Gln Arg Ala Ser Ala Arg Leu Pro Ser Thr Val Glu Ile Glu Thr
 340 345 350
 Ser Ala Asp Leu
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<210> 5

<211> 68
 <212> PRT
 <213> Mus muscalis

<400> 5
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 20 25 30
 Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly Phe Tyr
 35 40 45
 Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu Thr Ile
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 Asp Arg Tyr Leu
 65

<210> 6
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> The amino acid at position 1 can be S or T or A or
 L or I or V or M or F or Y or W or C

<221> VARIANT
 <222> (2)...(2)
 <223> The amino acid at position 2 can be S or T or A or
 N or P or D or E

<221> VARIANT
 <222> (3)...(3)
 <223> The amino acid at position 3 can not be E or D or
 P or K or R or H

<223> The amino acid at position 4 and at position 5 can
 be any amino acid

<221> VARIANT
 <222> (6)...(6)
 <223> The amino acid at position 6 can be I or V or M or
 N or Q or G or A

<223> The amino acid at position 7 and at position 8 can
 be any amino acid

<221> VARIANT
 <222> (9)...(9)
 <223> The amino acid at position 9 can be I or V or M or
 F or T

<221> VARIANT
 <222> (10)...(10)
 <223> The amino acid at position 10 can be S or T or A or
 N or C

<221> VARIANT
 <222> (11)...(11)
 <223> The amino acid at position 11 can be I or V or M
 or F or Y or W or S or T or A or C

<221> VARIANT
 <222> (12)...(12)
 <223> The amino acid at position 12 can be E or N or H

<221> VARIANT
 <222> (14)...(14)
 <223> The amino acid at position 14 can be Y or W or C
 or S or H

<223> The amino acid at position 15 and at position 16
 can be any amino acid

<221> VARIANT
 <222> (17)...(17)
 <223> The amino acid at position 17 can be I or V or M

<400> 6
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